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Assessment of Genetic Variability, Heritability and Genetic Advance in Field Pea (*Pisum sativum* L.) under Heat Stress Across Different Sowing Conditions

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ABSTRACT

Background: Field pea (*Pisum sativum* L.) productivity is severely affected by terminal heat stress, particularly under late sown conditions. Therefore, understanding genetic variability for yield and its contributing traits is important for developing heat-tolerant and high-yielding genotypes.

Methods: The experimental material comprised 55 genotypes, including 10 parental lines and 45 F_1 hybrids developed through a half-diallel mating design. The material was evaluated under timely- and late-sown environments during two *Rabi* seasons using RBD with three replications. Eleven agronomic traits were recorded and the data were analyzed for genetic variability, heritability, correlation and path coefficients to identify traits association with seed yield.

Result: The analysis of variance showed significant differences among the evaluated genotypes for all measured traits under both sowing conditions, confirming the existence of ample genetic variation. PCV were consistently greater than GCV, indicated that environmental factors influenced trait expression. Biological yield/plant, seed yield/plant, pods/plant and secondary branches/plant showed high heritability with substantial genetic advance, suggesting good prospects for selection. Seed yield/plant showed favourable associations with biological yield/plant, pods/plant, seeds/pod and seed index, whereas days to flowering and days to maturity were negatively associated with seed yield/plant. Path analysis highlighted biological yield/plant (timely sowing) and pods/plant (late sowing) as the direct contributors to seed yield/plant.

Key words: Correlation analysis, Field pea, Genetic advance, Genetic variability, Heritability, Path coefficient, Terminal heat stress.

INTRODUCTION

Field pea (*Pisum sativum* L.) is a cool-season crop that provides nutrition for people and feed for livestock. Its yield is often reduced by environmental stresses, especially heat (Dave *et al*., 2024). High temperatures during the reproductive stage are particularly harmful, even though the crop is grown in climates from semi-arid to temperate regions with the temperatures (7-30)°C (Olle *et al*., 2020). Heat stress disrupts processes like photosynthesis, pollen function, fertilization and pod development, which lowers yield (Kumar *et al*., 2025). The problem is more in late sowing, when flowering and seed filling coincide with high temperatures, causing major yield losses. Studying genetic variation and trait interactions under heat stress is key to developing better, heat-tolerant varieties.

Sufficient genetic variability enables the selection of superior genotypes. Assessing this variation helps breeders identify desirable parents and formulate effective selection strategies. Parameters such as GCV, PCV, heritability and genetic advance provide valuable information on the nature of variability and the expected response to selection. These parameters help to identify traits that are more likely to respond to selection. Correlation analysis identifies the association of seed yield with its related traits, whereas path coefficient analysis separates these associations into direct and indirect effects, thereby identifying characters that contribute most effectively to yield

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improvement (Singh and Kumar, 2023). Such information is particularly useful when selecting traits for simultaneous improvement under contrasting environments.

In this context, the present investigation focused on evaluating genetic variability, heritability, correlation and path coefficients for yield and its associated traits in ten parental lines and their forty-five F_1 hybrids under timely and late-sown conditions. The findings are expected to facilitate the identification of key traits for developing high-yielding and heat-tolerant field pea genotypes.

MATERIALS AND METHODS

The experimental trials were conducted across two *Rabi* seasons (2023-24 and 2024-25). In the first season, ten selected field pea genotypes were crossed using a half-diallel design to produce 45 F_1 hybrids. In the next season, these hybrids and their parents were tested under timely (5 Nov 2024) and late sowing (5 Dec 2024) in RBD with three replications at the research farm of Genetics and Plant Breeding Research, Acharya Narendra Deva University of Agriculture and Technology. Meteorological parameters, including maximum and minimum temperature, relative humidity, rainfall and other weather variables recorded during the crop growth period, were collected from the university meteorological observatory and are illustrated in Fig 1a and 1b.

Late sowing exposed the crop to higher temperatures during reproduction, causing heat stress. Data were recorded on five randomly selected plants for eleven characters, namely days to flowering, days to maturity, primary branches/plant, secondary branches/plant, plant height, pods/plant, seeds/pod, harvest index, seed index, Biological yield/plant and seed yield/plant. The recorded data were subjected to ANOVA and other statistical analyses using R software.

RESULTS AND DISCUSSION

Analysis of variance

ANOVA for eleven morpho-agronomic traits under timely-sown (Table 1) and late-sown (Table 2) conditions indicated significant genotypic differences, demonstrating considerable genetic variability within the experimental material. Considerable variation among the evaluated genotypes was observed for flowering time, maturity, plant height, pods/plant, biological yield/plant, harvest index and seed yield/plant, highlights the existence of diverse genetic backgrounds, Consequently, this offers considerable scope

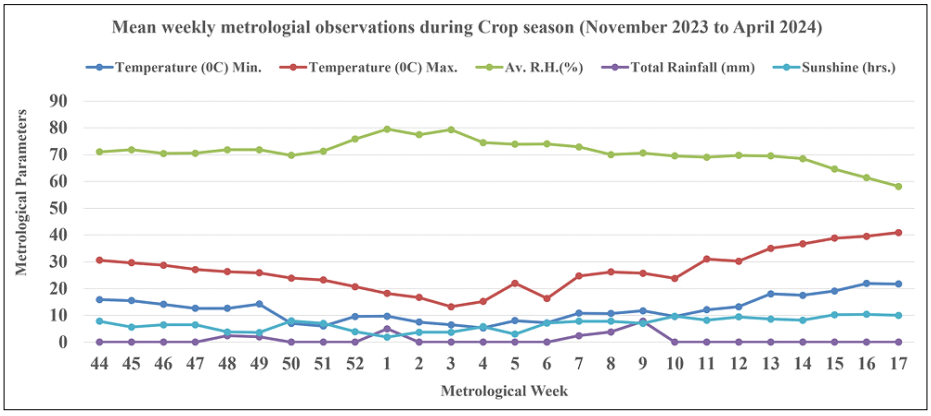


Fig 1a: Metrological observation in 2023-24.

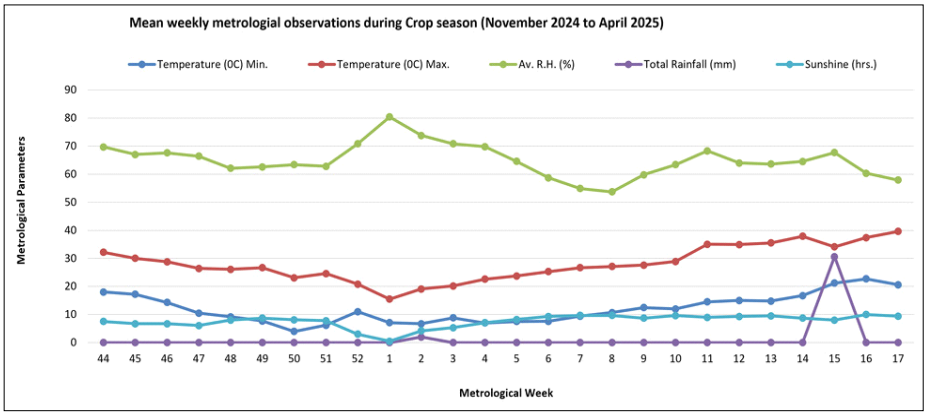


Fig 1b: Metrological data in 2024-25.

for selecting superior genotypes. and successful crop improvement programme.

GCV, PCV, heritability and genetic advance

Table 3 and 4 indicate that PCV were consistently greater than GCV across all the studied traits in both environments, reflecting the involvement of environmental factors. High PCV and GCV estimates were observed for seed yield, secondary branches/plant, biological yield/plant and pods/plant, reflecting considerable variation for these characters. Similar observations have been noted by Afreen *et al.* (2017) and Sharma *et al.* (2023). Conversely, days to maturity exhibited the least variability in both environments. The small differences between GCV and PCV for traits such as biological yield/plant, seed yield/plant and plant height suggests stronger genetic control with minimal environmental effects, whereas larger differences noted for harvest index and seeds/pod, indicate greater environmental sensitivity.

Heritability and genetic advance exhibited considerable variation among the studied traits under both timely and late-sown environments, reflecting differences in their underlying genetic regulation. Higher heritability values were obtained for biological yield/plant, plant height, seed yield/plant, pods/plant, secondary branches/plant and seed index, which suggests that the observed phenotypic differences were mainly explained by genetic factors. In comparison, days to flowering, days to maturity, primary branches/plant and harvest index expressed moderate heritability, whereas seeds/pod displayed relatively lower heritability, suggesting a stronger influence of environmental conditions on its expression.

Genetic advance estimates varied considerably among the evaluated traits. Biological yield/plant recorded the high genetic advance in both environments, followed by seed yield/plant, pods/plant and secondary branches/plant. Similar observations have been reported by Singh *et al.* (2019). The simultaneous occurrence of high heritability and genetic advance for traits including Biological yield/plant, seed yield/plant, pods/plant and secondary branches/plant indicates that substantial improvement can be obtained through phenotypic selection, making them useful

Table 1: Anova of half-diallel crossing and parents for 11 field pea traits in timely sown condition.

Source of variation	Replications	Treatments	Parents	Hybrids	Parents vs Hybrids	Error
Df	2	54	9	44	1	108
DTF	0.806	23.406**	35.274**	19.042**	108.627**	1.540
DTM	3.278	32.024**	46.033**	23.812**	267.3**	2.821
PH	4.671	246.228**	592.265**	172.935**	356.789**	4.258
PB	0.0064	0.287**	0.409**	0.193**	3.334**	0.027
SB	0.0012	1.477**	2.231**	0.849**	22.308**	0.038
PPP	4.628	40.051**	41.562**	16.526**	1061.533**	1.922
SPP	0.030	0.303**	0.276**	0.254**	2.683**	0.097
SI	0.185	4.692**	7.15**	3.434**	37.923**	0.184
BYPP	1.573	452.985**	602.261**	169.395**	11587.427**	3.413
HI	1.604	29.959**	41.924**	23.543**	204.577**	2.537
SYPP	1.32602	88.777**	80.352**	31.563**	2682.028**	1.701

Df: Degree of freedom, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, PB: Primary branches/plant, SB: Secondary branches/plant, PPP: Pods/plant, SPP: Seeds/pod, SI: Seed index, BYPP: Biological yield/plant, HI: Harvest index, SYPP: Seed yield/plant.

Table 2: Anova of half-diallel crossing and parents for 11 field pea traits in late sown condition.

Source of variation	Replications	Treatments	Parents	Hybrids	Parents vs Hybrids	Error
Df	2	54	9	44	1	108
DTF	0.709	21.2593**	34.7259**	16.4842**	110.163**	1.690
DTM	0.806	23.655**	30.7259**	15.1246**	335.3549**	2.330
PH	3.068	222.5057**	514.0253**	165.6972**	98.4001**	3.956
PB	0.014	0.3092**	0.5102**	0.2201**	2.4212**	0.017
SB	0.038	0.8364**	1.3311**	0.703**	2.2529**	0.052
PPP	1.272	33.4622**	69.5404**	6.7857**	882.524**	1.665
SPP	0.045	0.3138**	0.5961**	0.2553**	0.3448*	0.082
SI	0.187	3.8791**	7.3601**	3.1556**	4.384**	0.143
BYPP	2.440	419.7451**	767.5349**	175.1256**	8052.8949**	2.711
HI	8.133	36.5725**	60.7988**	32.4278**	0.9015	3.813
SYPP	2.094	51.3416**	113.0856**	18.9411**	921.2669**	1.447

Table 3: Mean and range of variability of parents and half-diallel crosses for 11 characters of field pea in timely sown condition.

Characters	Mean ± SEM	Range		GV	PV	EV	GCV	PCV	ECV	Heritability broad sense	Genetic advance	Genetic advance as percentage of mean
		Min	Max									
DTF	69.07±0.71	64	77	7.28	8.82	1.54	3.9	4.3	1.79	0.82	5.05	7.31
DTM	108.33±0.96	102	120	9.73	12.55	2.82	2.88	3.27	1.55	0.77	5.65	5.22
PH	106.69±1.19	82.4	118.4	80.65	84.91	4.25	8.41	8.63	1.93	0.94	18.03	16.89
PB	2.74±0.09	1.8	3.6	0.08	0.11	0.02	10.72	12.28	5.98	0.76	0.52	19.27
SB	4.62±0.11	2	6.4	0.47	0.51	0.03	14.98	15.58	4.26	0.92	1.37	29.7
PPP	27.28±0.8	14.2	33.4	12.7	14.63	1.92	13.06	14.01	5.08	0.86	6.84	25.08
SPP	6±0.18	5	7	0.06	0.16	0.09	4.35	6.77	5.18	0.41	0.34	5.77
SI	19.05±0.24	16.063	22.37	1.5	1.68	0.18	6.43	6.81	2.25	0.89	2.38	12.5
BYPP	80.3±1.06	39.191	99.3	149.85	153.27	3.41	15.24	15.41	2.3	0.97	24.93	31.04
HI	38.99±0.91	27.2808	44.844328	9.14	11.67	2.53	7.75	8.76	4.08	0.78	5.51	14.13
SYPP	31.33±0.75	13.686	40.413	29.02	30.72	1.7	17.19	17.69	4.16	0.94	10.78	34.42

Table 4: Mean and range of variability of parents and half-diallel crosses for 11 characters of field pea in late sown condition.

Characters	Mean ± SEM	Range		GV	PV	EV	GCV	PCV	ECV	Heritability broad sense	Genetic advance	Genetic advance as percentage of mean
		Min	Max									
DTF	65±0.75	59	73	6.52	8.21	1.69	3.93	4.41	2.00	0.79	4.69	7.21
DTM	102.37±0.88	96	113	7.11	9.44	2.33	2.60	3.00	1.49	0.75	4.77	4.66
PH	100.91±1.14	79	113.6	72.85	76.81	3.96	8.46	8.68	1.97	0.95	17.12	16.97
PB	2.55±0.07	1.4	3.6	0.10	0.11	0.02	12.23	13.27	5.15	0.85	0.59	23.22
SB	3.48±0.13	0.8	4.8	0.26	0.31	0.05	14.69	16.08	6.56	0.83	0.96	27.63
PPP	24.42±0.74	12.2	31.8	10.60	12.26	1.67	13.33	14.34	5.28	0.86	6.23	25.53
SPP	5.72±0.16	4.8	6.8	0.08	0.16	0.08	4.85	6.98	5.02	0.48	0.40	6.94
SI	16.15±0.21	13.42	21.41	1.25	1.39	0.14	6.91	7.29	2.34	0.90	2.18	13.47
BYPP	65.36±0.95	26.49	89.82	139.01	141.72	2.71	18.04	18.21	2.52	0.98	24.05	36.80
HI	34.87±1.12	27.6	45.39	10.92	14.73	3.81	9.47	11.01	5.60	0.74	5.86	16.80
SYPP	22.67±0.69	10.99	33.70	16.63	18.08	1.45	17.99	18.75	5.31	0.92	8.06	35.54

Table 5: Genotypic (Upper diagonal) and phenotypic (Lower diagonal) correlation coefficient of 11 traits in timely sown condition.

Characters	DTF	DTM	PH	PB	SB	PPP	SPP	SI	BYPP	HI	SYPP
DTF	1**	0.6912**	-0.4701**	-0.3884**	-0.3499**	-0.4021**	-0.1182	-0.2146	-0.3604**	-0.1829	-0.4068**
DTM	0.5427**	1**	-0.3578**	-0.3374*	-0.3173*	-0.4994**	-0.1265	-0.0696	-0.3971**	-0.1751	-0.424**
PH	-0.4156**	-0.328**	1**	0.2776*	0.5661**	0.2359 NS	0.2532	0.1555	0.3508**	-0.0757	0.2779*
PB	-0.2641**	-0.2402**	0.2281**	1**	0.6633**	0.6857**	0.2261	0.6097**	0.6757**	0.4001**	0.7554**
SB	-0.3171**	-0.2624**	0.5206**	0.564**	1**	0.6161**	0.4821**	0.522**	0.72**	0.2555	0.7357**
PPP	-0.3598**	-0.3784**	0.2194**	0.5338**	0.5429**	1**	0.4939**	0.2582	0.8428**	0.4323**	0.9185**
SPP	-0.0352	-0.1488	0.1647*	0.1695*	0.2851**	0.105	1**	0.0687	0.5355**	0.3441*	0.6253**
SI	-0.2102**	-0.0462	0.137	0.4943**	0.4598**	0.2214**	0.0145	1**	0.4898**	0.2856*	0.548**
BYPP	-0.3334**	-0.3618**	0.3413**	0.5928**	0.6859**	0.7762**	0.3607**	0.4679**	1**	0.071	0.8947**
HI	-0.1522	-0.1075	-0.0623	0.2842**	0.1763*	0.4135**	0.2833**	0.2762**	0.0466 NS	1**	0.506**
SYPP	-0.3702**	-0.3625**	0.2664**	0.6355**	0.6716**	0.8599**	0.4507**	0.5301**	0.8711**	0.5274**	1**

Table 6: Genotypic (Upper diagonal) and phenotypic (Lower diagonal) correlation coefficient of 11 traits in late sown condition.

Characters	DTF	DTM	PH	PB	SB	PPP	SPP	SI	BYPP	HI	SYPP
DTF	1 **	0.6159 **	-0.4503 **	-0.4696 **	-0.3874 **	-0.4818 **	-0.1479	-0.245	-0.3858 **	-0.1608	-0.4764 **
DTM	0.4482 **	1 **	0.0058	-0.254	-0.0139	-0.4289 **	-0.0824	-0.1206	-0.3079 *	-0.1866	-0.3702 **
PH	-0.3868 **	0.0096	1 **	0.2384	0.5051 **	0.3585 **	0.2282	0.2967 *	0.3772 **	0.0927	0.4113 **
PB	-0.4019 **	-0.2334 **	0.2137 **	1 **	0.6759 **	0.6171 **	0.2376	0.6219 **	0.6222 **	0.1287	0.7332 **
SB	-0.3096 **	-0.0193	0.4408 **	0.5766 **	1 **	0.5283 **	0.2707 *	0.543 **	0.4741 **	0.2796 *	0.6419 **
PPP	-0.4178 **	-0.3192 **	0.322 **	0.5145 **	0.462 **	1 **	0.3959 **	0.2246	0.8162 **	0.0802	0.8751 **
SPP	-0.0811	-0.1158	0.1647 *	0.1486	0.1738 *	0.1303	1 **	0.2208	0.5086 **	0.2203	0.6401 **
SI	-0.1978 *	-0.0903	0.2686 **	0.5492 **	0.483 **	0.1973 *	0.086	1 **	0.467 **	0.2244	0.5868 **
BYPP	-0.3439 **	-0.2879 **	0.3583 **	0.5634 **	0.4267 **	0.7506 **	0.3565 **	0.4394 **	1 **	-0.2867 *	0.8725 **
HI	-0.1257	-0.0994	0.0839	0.1018	0.2441 **	0.1613 *	0.2293 **	0.2154 **	-0.2726 **	1 **	0.2039
SYPP	-0.4121 **	-0.3048 **	0.3838 **	0.64 **	0.5774 **	0.837 **	0.4984 **	0.5531 **	0.8301 **	0.296 **	1 **

targets in a field pea breeding programme, particularly under late-sown conditions where heat stress limits productivity.

Correlation coefficient

Table 5 and 6 showed the pattern of trait associations remained largely consistent across both sowing conditions. Similar trends have been reported by Singh *et al.* (2017). Seed yield exhibited favourable associations with most of the yield contributing traits under both environments. In contrast, days to flowering and days to maturity were negatively associated with seed yield/plant, suggesting that early-flowering and early-maturing genotypes possess greater potential to perform better under terminal heat stress, particularly in late-sown conditions.

Genotypic correlations were generally stronger than the corresponding phenotypic correlations, indicating that genetic factors contributed more strongly to trait associations than environmental effects. Days to flowering showed a positive relationship with days to maturity, whereas both traits were negatively associated with plant height, pods/plant, biological yield/plant and seed yield/ plant, suggesting that genotypes with early flowering and maturity are more productive, especially under late sown conditions.

Days to flowering displayed a positive relationship with days to maturity, whereas it showed significant negative associations with plant height, primary branches/plant, pods/plant, biological yield/plant and seed yield/plant. Likewise, days to maturity was negatively correlated with pods/plant, Biological yield/plant and seed yield/plant,

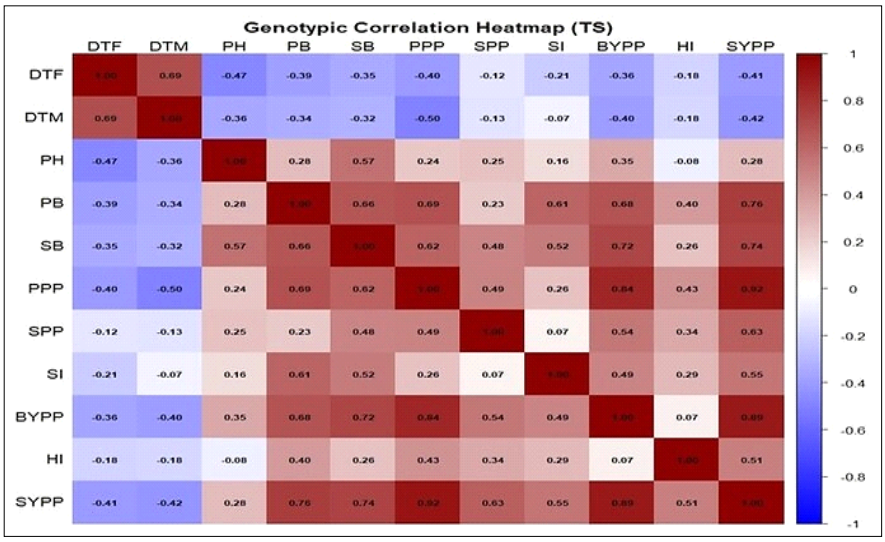


Fig 2a: Genotypic correlation heatmap of 11 traits of field pea under timely sown condition.

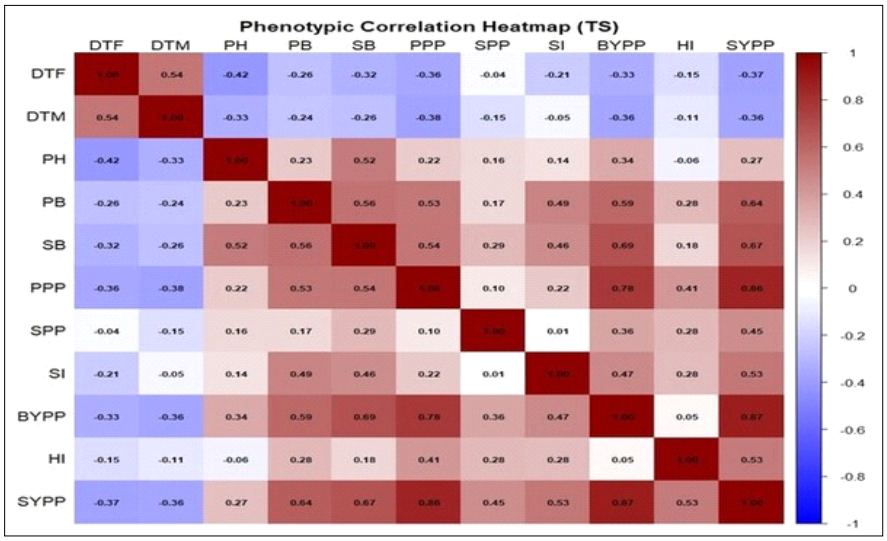


Fig 2b: Phentypic correlation heatmap of 11 traits in field pea under timely sown condition.

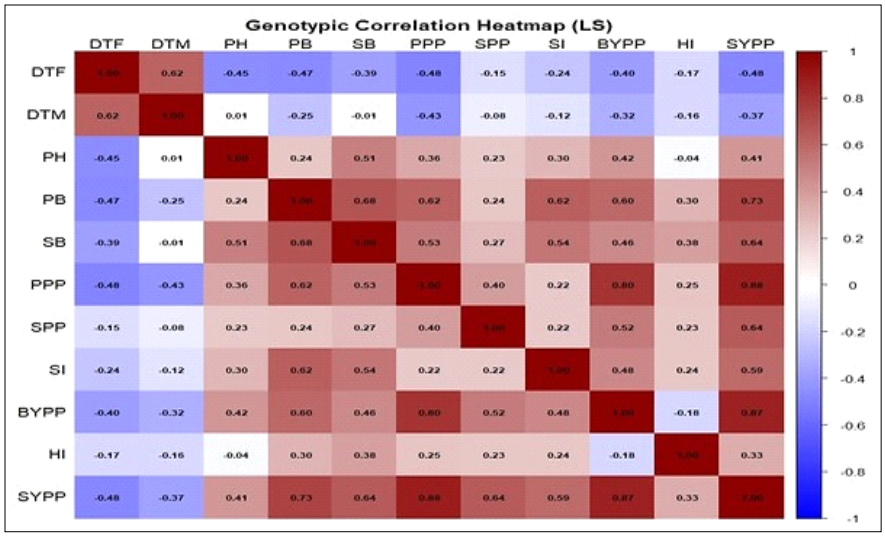


Fig 3a: Genotypic correlation heatmap of 11 traits of field pea under late sown condition.

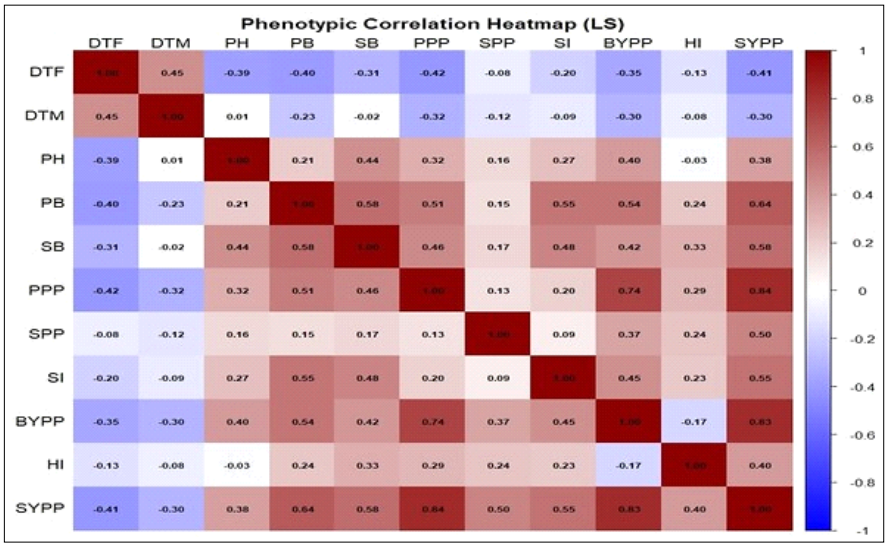


Fig 3b: Genotypic correlation heatmap of 11 traits of field pea under late sown condition.

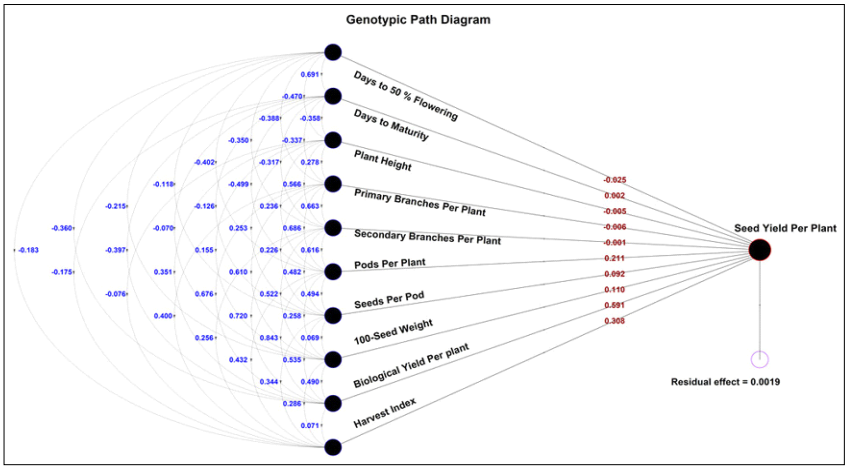


Fig 4a: Genotypic path coefficient under timely sown condition.

reflecting the advantage of early phenological development to improve productivity, Similar findings were reported by Kumar *et al.* (2014).

Furthermore, Biological yield/plant maintained strong positive relationships with pods/plant, seeds/pod, primary branches/plant, secondary branches/plant and seed yield/plant in both the environments. These associations emphasize the role of biomass production in determining seed yield/plant. Harvest index also exhibited positive relationships with seed yield/plant under timely sowing;

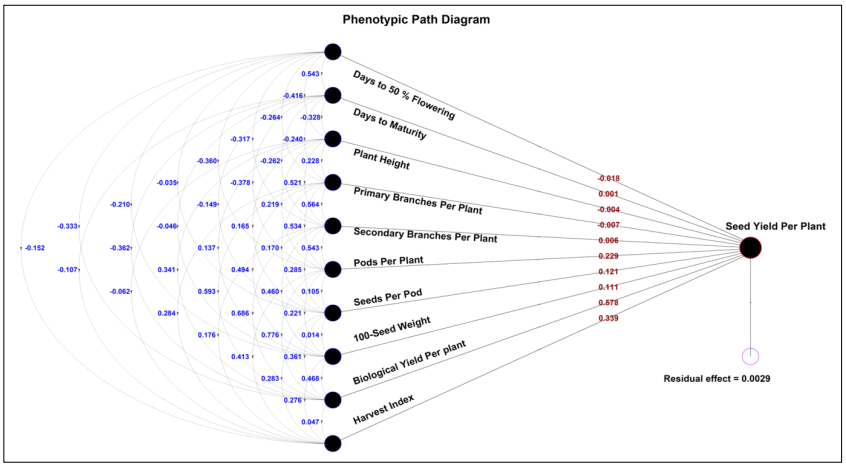


Fig 4b: Phenotypic Path coefficient under timely sown condition.

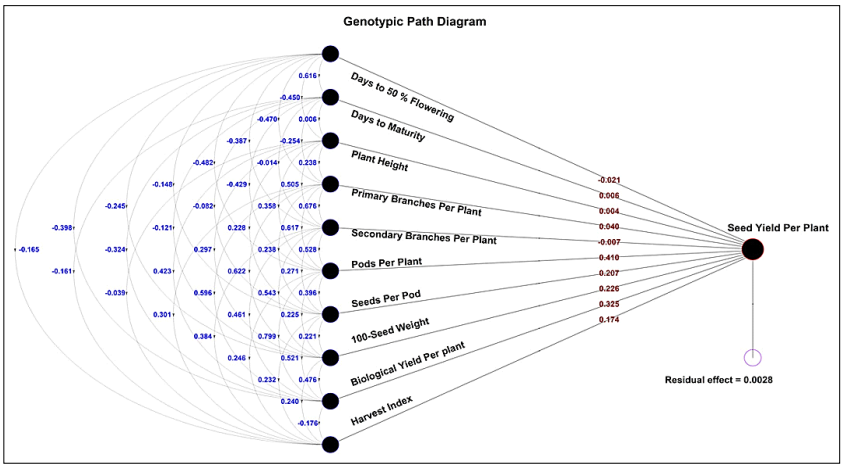


Fig 5a: Genotypic path coefficient under late sown condition.

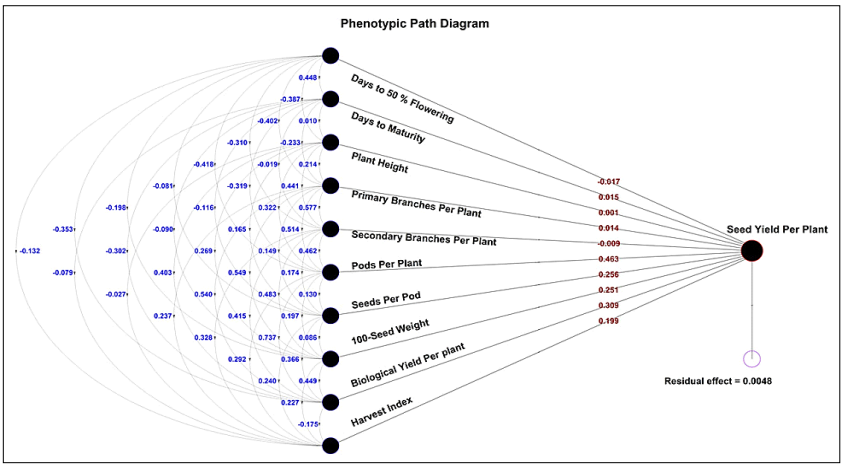


Fig 5b: Phenotypic path coefficient under late sown condition.

Table 7: Genotypic and phenotypic path coefficient of field pea in timely sown condition.

Characters		DTF	DTM	PH	PB	SB	PPP	SPP	SI	BYPP	HI
DTF	G	-0.02476	0.00144	0.00216	0.0024	0.00038	-0.08468	-0.01083	-0.02353	-0.213	-0.05639
	P	-0.01812	0.00065	0.00155	0.00192	-0.00189	-0.08253	-0.00428	-0.02333	-0.1926	-0.05159
DTM	G	-0.01711	0.00209	0.00165	0.00209	0.00035	-0.10517	-0.01159	-0.00763	-0.23472	-0.05399
	P	-0.00983	0.0012	0.00122	0.00175	-0.00157	-0.08682	-0.01788	-0.00514	-0.209	-0.03643
PH	G	0.01164	-0.00075	-0.0046	-0.00172	-0.00062	0.04967	0.02321	0.01705	0.20732	-0.02333
	P	0.00753	-0.00039	-0.00373	-0.00166	0.00311	0.05034	0.01985	0.01521	0.19716	-0.02112
PB	G	0.00962	-0.0007	-0.00128	-0.00618	-0.00072	0.1444	0.02072	0.06687	0.39935	0.12338
	P	0.00479	-0.00029	-0.00085	-0.00728	0.00337	0.12245	0.02018	0.0547	0.34244	0.09609
SB	G	0.00866	-0.00066	-0.0026	-0.0041	-0.00109	0.12975	0.04419	0.05724	0.42555	0.0788
	P	0.00574	-0.00032	-0.00194	-0.0041	0.00598	0.12454	0.03454	0.05105	0.39622	0.05979
PPP	G	0.00996	-0.00104	-0.00109	-0.00424	-0.00067	0.21059	0.04526	0.02832	0.49812	0.13332
	P	0.00652	-0.00046	-0.00082	-0.00388	0.00324	0.22944	0.01261	0.02458	0.44839	0.14018
SPP	G	0.00293	-0.00026	-0.00117	-0.0014	-0.00053	0.10401	0.09164	0.00754	0.31648	0.1061
	P	0.00064	-0.00018	-0.00061	-0.00122	0.00171	0.024	0.12069	0.00168	0.20831	0.09598
SI	G	0.00531	-0.00015	-0.00072	-0.00377	-0.00057	0.05439	0.0063	0.10966	0.28952	0.08808
	P	0.00381	-0.00006	-0.00051	-0.00358	0.00275	0.0508	0.00182	0.11102	0.27035	0.09361
BYPP	G	0.00892	-0.00083	-0.00161	-0.00418	-0.00079	0.17749	0.04907	0.05372	0.59104	0.0219
	P	0.00604	-0.00044	-0.00127	-0.00431	0.0041	0.17809	0.04347	0.05196	0.57767	0.01579
HI	G	0.00453	-0.00037	0.00035	-0.00247	-0.00028	0.09105	0.03153	0.03132	0.04198	0.30837
	P	0.00276	-0.00013	0.00023	-0.00206	0.00105	0.09489	0.03414	0.03067	0.02692	0.33893

Residual genotypic = 0.0019.

Residual phenotypic = 0.0029.

G: Genotypic, P: Phenotypic, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, PB: Primary branches/plant, SB: Secondary branches/plant, PPP: Pods/plant, SPP: Seeds/pod, SI: Seed index, BYPP: Biological yield/plant, HI: Harvest index, SYPP: Seed yield/plant.

Table 8: Genotypic and phenotypic path coefficient of field pea in late sown condition.

Characters		DTF	DTM	PH	PB	SB	PPP	SPP	SI	BYPP	HI
DTF	G	-0.02437	0.00552	0.00787	-0.01854	-0.00102	-0.26172	-0.03714	-0.07082	-0.06318	-0.01298
	P	-0.0176	0.00904	0.00743	-0.00845	0.00108	-0.23581	-0.02437	-0.05822	-0.06918	-0.01602
DTM	G	-0.01501	0.00896	-0.0001	-0.01003	-0.00004	-0.23297	-0.0207	-0.03486	-0.05043	-0.01506
	P	-0.00789	0.02016	-0.00018	-0.00489	0.00007	-0.18016	-0.03473	-0.02658	-0.05792	-0.01269
PH	G	0.01098	0.00005	-0.01748	0.00942	0.00133	0.19473	0.05731	0.08576	0.06177	0.00748
	P	0.00681	0.00019	-0.01921	0.00449	-0.00154	0.18174	0.04947	0.07906	0.07208	0.01071
PB	G	0.01145	-0.00228	-0.00417	0.03949	0.00178	0.33517	0.05965	0.17979	0.10189	0.01039
	P	0.00707	-0.00469	-0.0041	0.02092	-0.002	0.29039	0.04436	0.16159	0.11332	0.01306
SB	G	0.00944	-0.00012	-0.00883	0.02669	0.00263	0.28697	0.06799	0.15697	0.07764	0.02256
	P	0.00545	-0.00039	-0.00847	0.01209	-0.00348	0.26076	0.05232	0.14231	0.08586	0.03115
PPP	G	0.01174	-0.00384	-0.00627	0.02437	0.00139	0.54315	0.09943	0.06494	0.13366	0.00647
	P	0.00735	-0.00644	-0.00618	0.01082	-0.00161	0.56441	0.03902	0.05807	0.15099	0.02057
SPP	G	0.0036	-0.00074	-0.00399	0.00938	0.00071	0.21503	0.25116	0.06382	0.0833	0.01778
	P	0.00143	-0.00233	-0.00317	0.00311	-0.00061	0.07337	0.30073	0.02499	0.07172	0.02927
SI	G	0.00597	-0.00108	-0.00519	0.02456	0.00143	0.12201	0.05545	0.2891	0.07648	0.01811
	P	0.00348	-0.00182	-0.00516	0.01154	-0.00169	0.11136	0.02548	0.29424	0.08839	0.02747
BYPP	G	0.0094	-0.00276	-0.00659	0.02457	0.00125	0.44329	0.12775	0.135	0.16377	-0.02314
	P	0.00605	-0.00581	-0.00688	0.01184	-0.00149	0.42364	0.10701	0.12933	0.20117	-0.03476
HI	G	0.00392	-0.00167	-0.00162	0.00508	0.00074	0.04354	0.05533	0.06487	-0.04696	0.08069
	P	0.00221	-0.00201	-0.00161	0.00215	-0.00085	0.09104	0.06889	0.0634	-0.05484	0.12752

Residual genotypic = 0.0032.

Residual phenotypic = 0.0052.

however, these associations became comparatively weaker under late sown conditions, suggesting that its contribution declined under heat stress.

The consistent positive correlations among traits across studies highlight their usefulness for selection in improving seed yield/plant, particularly *via* pods/plant, seeds/pod and Seed index (Georgieva *et al*., 2015; Sharma *et al*., 2023). Pods/plant, biological yield/plant, primary branches/plant and secondary branches/plant were identified as major contributors to seed yield/plant under both timely and late-sown conditions, highlighting their usefulness in improving yield across different environments, especially under late sown stress conditions. Fig 2a and 2b present the genotypic and phenotypic correlation heatmaps, respectively, under timely-sown conditions, whereas Fig 3a and 3b depict the corresponding genotypic and phenotypic correlation heatmaps under late-sown conditions in field pea.

Path coefficients analysis

Path coefficient analysis was used to determine the relative contribution of individual traits to seed yield/plant by partitioning their correlations into direct and indirect effects. The results obtained under timely and late-sown environments are given in Table 7 and 8, while the corresponding genotypic and phenotypic path diagrams are illustrated in Fig 4 and 5. Under timely-sown conditions, biological yield/plant produced the strongest positive direct effect on seed yield/plant at genotypic and phenotypic levels, indicating that improvements in biomass production are predicted to enhance grain yield under favourable growing conditions. In contrast, its direct contribution was comparatively lower in late sown condition, where terminal heat stress altered the relative importance of yield components. Under late sown conditions, pods/plant made the greatest direct contribution to seed yield/plant. Seeds/pod and seed index also made comparatively greater direct contributions under heat-stress conditions than timely sown condition, highlighting their importance in maintaining productivity when plants are exposed to elevated temperatures during the reproductive stage. Harvest index contributed positively under timely sowing but its influence declined under late sowing, indicating that its effectiveness was reduced under stress conditions.

Days to flowering exerted a negative direct effect on seed yield/plant under both environments, suggesting that earlier flowering genotypes possess a greater capacity to maintain productivity, particularly when exposed to terminal heat stress. Examination of indirect effects further showed that several traits influenced seed yield/plant indirectly through biological yield/plant under late sown conditions, however, pods/plant and seeds/pod represented the major indirect contributors to yield improvement.

The residual effects were relatively low under both environments, suggesting that the characters included in the analysis captured most of the variability observed in seed yield/plant. Overall, the results emphasize that biomass related traits are more important under favourable environments, whereas reproductive attributes, particularly pods/plant and seeds/pod, become increasingly important under late sown, heat-stressed conditions. Similar observations have been reported by Tofiq *et al.* (2015).

CONCLUSION

The present investigation demonstrated the considerable genetic diversity among the evaluated field pea genotypes under timely and late sown environments, indicating good prospects for genetic improvement. Although environmental factors influenced the expression of all the studied traits, biological yield/plant, seed yield/plant, pods/plant and secondary branches/plant consistently exhibited favourable genetic parameters, suggesting that these characters can be improved effectively through selection. Correlation and path coefficient analyses further identified biological yield/plant, pods/plant, seeds/pod and seed index as the main contributors to seed yield/plant. Under heat stress conditions, reproductive traits, particularly pods/plant and seeds/pod, assumed greater importance in determining yield performance. Therefore, these may be serve as valuable traits for developing high-yielding and heat tolerant field pea cultivars suitable for both timely and late sown environments.

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Conflict of interest

The author declares that there are no conflicts of interest regarding the publication of this article, No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

REFERENCES

Afreen, S., Singh, A.K., Moharana, D.P., Singh, V., Singh, P. and Singh, B. (2017). Genetic evaluation for yield and its attributes in garden pea (*Pisum sativum* L.) under North Indian gangetic plain conditions. *Int. J. Curr. Microbiol. App. Sci.* **6(2):** 1399-1404.

Dave, K., Kumar, A., Dave, N., Jain, M., Dhanda, P.S., Yadav, A. and Kaushik, P. (2024). Climate change impacts on legume physiology and ecosystem dynamics: A multifaceted perspective. *Sustainability*. **16(14):** p.6026.

Georgieva, N., Nikolova, I. and Kosev, V. (2015). Association study of yield and its components in pea (*Pisum sativum* L.). *Int. J. Pharmacogn.* **2:** 536-542.

Kumar, A., Muthuramalingam, P., Kumar, R., Tiwari, S., Verma, L., Park, S. and Shin, H. (2025). Adapting crops to rising temperatures: Understanding heat stress and plant resilience mechanisms. *International Journal of Molecular Sciences.* **26(21):** p.10426.

Kumar, V., Singh, J. and Srivastava, C.P. (2014). Genetic variability, correlation and path analysis based on seed yield attributes traits in diverse genotypes of pea (*Pisum sativum* L.). *Environment and Ecology*. **32(3):** 1019-1024.

Olle, M., Williams, I.H., Rosa, E. and Tamm, S. (2020). Finding best field pea (*Pisum sativum* L.) cultivars for breeding in Northern climatic conditions. *Acta Agriculturae Scandinavica, Section B-Soil and Plant Science*. **70(1):** 1-7.

Sharma, S., Bhushan, A., Samnotra, R.K., Kumar, B., Wani, O.A., Naik, R. and Kumar, M. (2023). Genetic variability, correlation and path coefficient analysis in advanced matromorphic generations of garden pea (*Pisum sativum* L.). *Legume Research-An International Journal*. **48(8):** 1274-1280. doi: 10.18805/LR-5128.

Singh, M. and Kumar, P. (2023). Genetic diversity in lentil germplasm: Implications for breeding. *Plant Genetic Resources Journal*. **21(1):** 55-63.

Singh, N. (2017). Pulses: An overview. *J. food Sci. and Tech.* **54(4):** 853-857.

Singh, S., Verma, V., Singh, B., Sharma, V.R. and Kumar, M. (2019). Genetic variability, heritability and genetic advance studies in pea (*Pisum sativum* L.) for quantitative characters. *Indian Journal of Agricultural Research*. **53(5):** 542-547. doi: 10.18805/IJARe.A-5245.

Tofiq, S.E., Abdulkhaleq, D.A., Amin, T.N.H. and Azez, O.K. (2015). Correlation and path coefficient analysis in seven field pea (*Pisum sativum* L.) genotypes created by half diallel analysis in sulaimani region for F_2 generation. *International Journal of Plant, Animal and Environmental Sciences.* **5(4):** 93-97.